

- <110> McCall, Catherine A. Hunter, Shirley Wu Weber, Eric R.
- <120> NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
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- <140> not yet assigned
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- <150> 09/292,225
- <151> 1999-04-15
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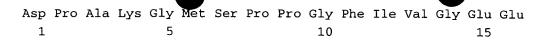
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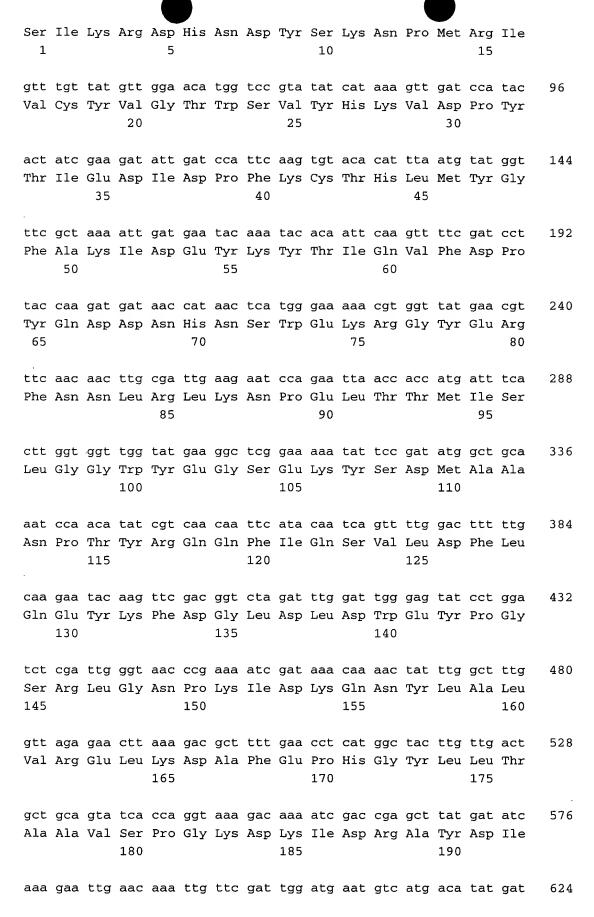
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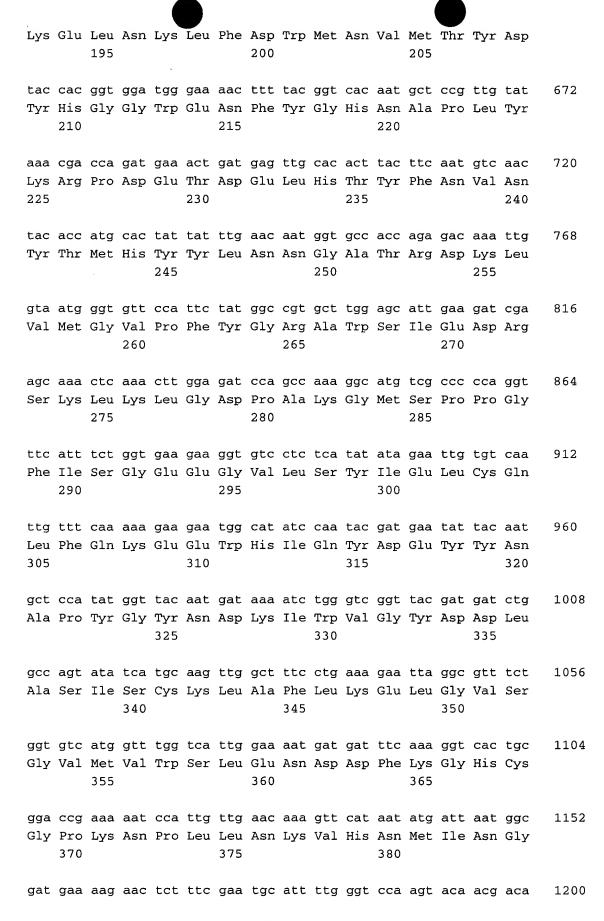
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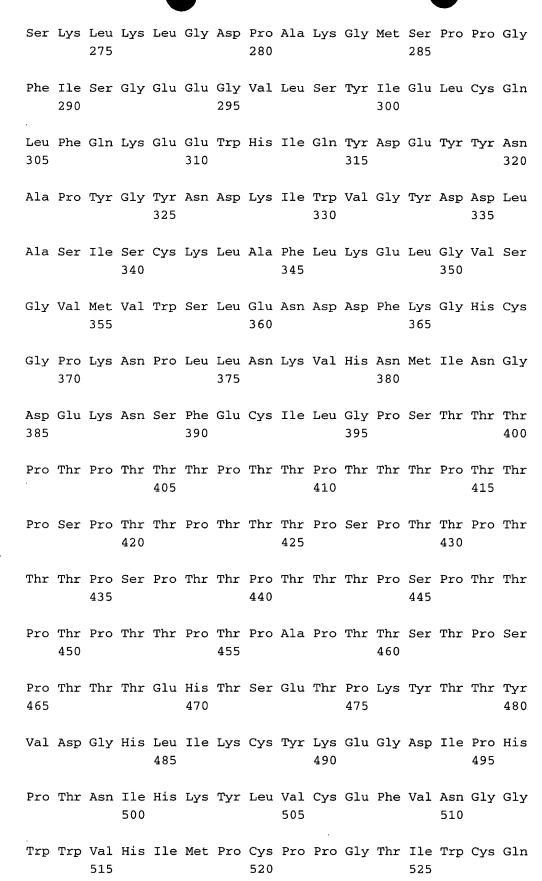
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					atc Ile				_	_		_				1488
					aaa Lys		_	_	_	_		-				1536
					atg Met											1584
_		_		_	ata Ile		_									1608
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Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val Phe Asp Pro Tyr Gln Asp Asp Asn His Asn Ser Trp Glu Lys Arg Gly Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Ile Gln Ser Val Leu Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr Leu Ala Leu Val Arg Glu Leu Lys Asp Ala Phe Glu Pro His Gly Tyr Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Arg Ala Tyr Asp Ile Lys Glu Leu Asn Lys Leu Phe Asp Trp Met Asn Val Met Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Phe Tyr Gly His Asn Ala Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile Glu Asp Arg



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<212> PRT

<213> Dermatophagoides farinae

<220>

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     Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro Met Met Ile
Ф
      1
                       5
                                          10
m
[7]
    Val Xaa Tyr Gly Gly Ser Ser Gly Tyr Gln Ser Xaa Lys Arg Xaa Xaa
20
                                      25
                                                          30
    Thr
Ħ
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    <211> 31
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    <213> Artificial Sequence
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     <223> Description of Artificial Sequence: Synthetic
          Primer
     <220>
     <223> At location 24, n = a, c, t or g
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<212> DNA

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     <213> Artificial Sequence
     <223> Description of Artificial Sequence: Synthetic
           Primer
<220>
ıÕ
     <223> At locations 12 and 21, n = a, c, t or g
M
Tur They they had and
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     ccttcttcac cnacratcaa ncc
                                                                          23
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Gln Ser Arg Asp Arg Asn Asp Lys Pro Tyr Xaa Ile Val Lys Lys

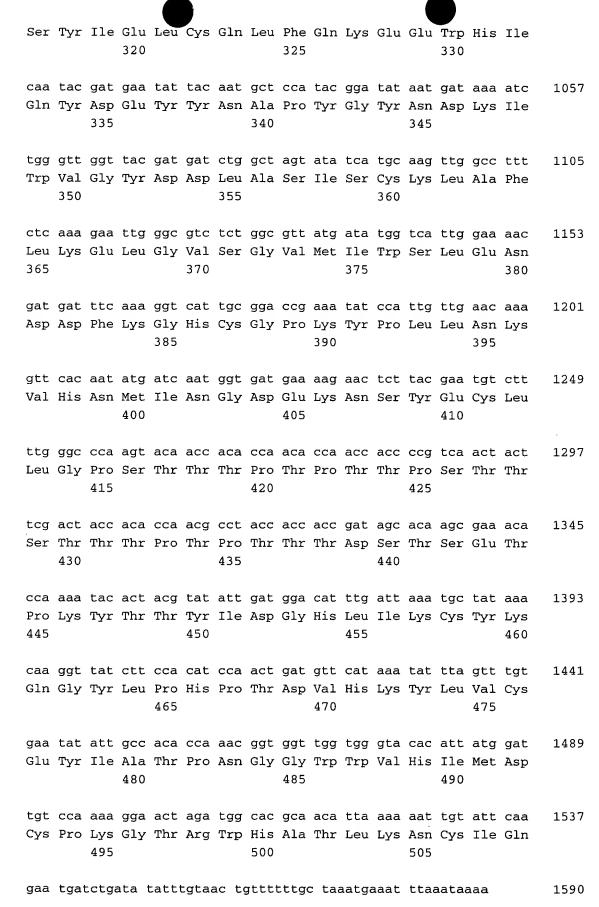
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15

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	<400)> 34	1														
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. ում ևով կան կուր												gat Asp					97
Anna Anga Anna Anna												gga Gly 40				_	145
Andrews and the second sections of the second		_										att Ile					193
allinelli allinelli												gat Asp					241
				-		_				-	_	aac Asn					289
												aga Arg					337
												tat Tyr 120				_	385
	aaa	tat	tcg	gat	atg	gca	gcc	aat	сса	aca	tat	cgt	cag	caa	ttt	gtt	433

				(
Lys 125	Tyr	Ser	Asp	Met	Ala 130	Ala	Asn	Pro	Thr	Tyr 135	Arg	Gln	Gln	Phe	Val 140	
		_	_	-		_	caa Gln	-				_			-	481
_	_		-				tca Ser			~~					~	529
							gtt Val 180	_	_				_		-	577
				_	_		gcc Ala	_	-					_		625
		_	_				aaa Lys	_	_			_		_		673
_		_	_			_	tac Tyr					-		_		721
			-	-	_		aaa Lys	_		-	-	_	_	_	_	769
					-		tac Tyr 260		_				_			817
							gtt Val									865
_		-		_	_	-	agc Ser		-				_	_	-	913
							ttt Phe									961
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Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu 50 55 60

Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val 65 70 75 80

Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp 115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu 130 135 140

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr 165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr 180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala

195 200 205

Ту	r Glu 210	Leu	Lys	Glu	Leu	Asn 215	Gln	Leu	Phe	Asp	Trp 220	Met	Asn	Val	Met
Th.	r Tyr 5	Asp	Tyr	His	Gly 230	Gly	Trp	Glu	Asn	Val 235	Phe	Gly	His	Asn	Ala 240
Pr	o Leu	Tyr	Lys	Arg 245	Pro	Asp	Glu	Thr	Asp 250	Glu	Leu	His	Thr	Tyr 255	Phe
As	n Val	Asn	Tyr 260	Thr	Met	His	Tyr	Tyr 265	Leu	Asn	Asn	Gly	Ala 270	Thr	Arg
As	o Lys	Leu 275	Val	Met	Gly	Val	Pro 280	Phe	Tyr	Gly	Arg	Ala 285	Trp	Ser	Ile
Gl [,]	a Asp 290	Arg	Ser	Lys	Val	Lys 295	Leu	Gly	Asp	Pro	Ala 300	Lys	Gly	Met	Ser
Pr:	o Pro	Gly	Phe	Ile	Thr 310	Gly	Glu	Glu	Gly	Val 315	Leu	Ser	Tyr	Ile	Glu 320
Le	ı Cys	Gln	Leu	Phe 325	Gln	Lys	Glu	Glu	Trp 330	His	Ile	Gln	Tyr	Asp 335	Glu
Ty	r Tyr	Asn	Ala 340	Pro	Tyr	Gly	Tyr	Asn 345	Asp	Lys	Ile	Trp	Val 350	Gly	Tyr
As	g Asp	Leu 355	Ala	Ser	Ile	Ser	Cys 360	Lys	Leu	Ala	Phe	Leu 365	Lys	Glu	Leu
Gl:	y Val 370	Ser	Gly	Val	Met	Ile 375	Trp	Ser	Leu	Glu	Asn 380	Asp	Asp	Phe	Lys
G1; 38	y His 5	Cys	Gly	Pro	Lys 390	Tyr	Pro	Leu	Leu	Asn 395	Lys	Val	His	Asn	Met 400
Il	e Asn	Gly	Asp	Glu 405	Lys	Asn	Ser	Tyr	Glu 410	Cys	Leu	Leu	Gly	Pro 415	Ser
Th	r Thr	Thr	Pro 420	Thr	Pro	Thr	Thr	Pro 425	Ser	Thr	Thr	Ser	Thr 430	Thr	Thr
Pr	o Thr	Pro 435	Thr	Thr	Thr	Asp	Ser 440	Thr	Ser	Glu	Thr	Pro 445	Lys	Tyr	Thr
Th	r Tyr	Ile	Asp	Gly	His	Leu	Ile	Lys	Cys	Tyr	Lys	Gln	Gly	Tyr	Leu

450 455 460

Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala 465 470 475 480

Thr Pro Asn Gly Gly Trp Trp Val His Ile Met Asp Cys Pro Lys Gly
485 490 495

Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu 500 505

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<211> 1621

<212> DNA

<213> Dermatophagoides farinae

<400> 36

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	atg	aat	gcg	gcc	act	aaa	cga	gat	caç	aat	aat	tat	tcg	aaa	aat	cca	96
	Met	Asn	Ala	Ala 20	Thr	Lys	Arg	Asp	His 25	Asn	Asn	Tyr	Ser	Lys 30	Asn	Pro	
	atg	cga	atc	gta	tgt	tat	gtt	gga	aca	tgg	tcc	gtt	tat	cat	aaa	gtt	144
in. En sun un vol vol en En U.	Met	Arg	Ile 35	Val	Cys	Tyr	Val	Gly 40	Thr	Trp	Ser	Val	Tyr 45	His	Lys	Val	
l	gat	cca	tac	aca	att	gaa	gat	att	gat	cct	ttc	aaa	tgt	act	cat	ttg	192
u D	Asp		Tyr	Thr	Ile	Glu		Ile	Asp	Pro	Phe		Cys	Thr	His	Leu	
a A		50					55					60,					
			ggt													_	240
	мес 65	TYL	Gly	Pne	Ата	ъуs 70	11e	Asp	GIU	туг	ъуs 75	туr	Thr	11e	GIN	80	
			cca														288
	Phe	Asp	Pro	Phe	Gln 85	Asp	Asp	Asn	His	Asn 90	Ser	Trp	Glu	Lys	His 95	Gly	
	tat	gaa	cgt	ttc	aac	aac	ttg	aga	ttg	aag	aat	cca	gaa	ttg	acc	acc	336
	Tyr	Glu	Arg		Asn	Asn	Leu	Arg		Lys	Asn	Pro	Glu		Thr	Thr	
				100					105					110			
	_		tca	_					_			-			~	•	384
	мес	IIe	Ser 115	Leu	GIY	GIĀ	Trp	120	GIU	GIY	Ser	GIU	Lys 125	туr	Ser	Asp	
	atg	gca	gcc	aat	cca	aca	tat	cgt	cag	caa	ttt	gtt	caa	tca	gtt	ttg	432
	Met	Ala 130	Ala	Asn	Pro	Thr	Tyr 135	Arg	Gln	Gln	Phe	Val 140	Gln	Ser	Val	Leu	
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Asp 145	Phe	Leu	Gln	Glu	Tyr 150	Lys	Phe	Asp	Gly	Leu 155	Asp	Leu	Asp	Trp	Glu 160	
						ggc					-					528
			_	_	_	ctt Leu			-		-					576
	_		_	_	_	tca Ser				-			_	_	_	624
				-	_	aac Asn 215		_		_		_		-	•	672
		_				gga Gly		_		-					_	720
_	_			_		gat Asp	-	_	_	_	_					768
	-				_	cac His			_				_		_	816
						gtt Val										864
			_		_	aaa Lys 295			_	_	_			_		912
						ggt Gly	_			_					_	960
						aaa Lys								_	_	1008
tat	tac	aat	gct	cca	tac	gga	tat	aat	gat	aaa	atc	tgg	gtt	ggt	tac	1056



Tyr	Tyr	Asn	Ala 340	Pro	Tyr	Gly	Tyr	Asn 345	Asp	Lys	Ile	Trp	Val 350	Gly	Tyr	
						tca Ser								_	_	1104
	_			_	_	ata Ile 375			_	_		_	•			1152
		_		_		tat Tyr		_	_			_			-	1200
						aac Asn									-	1248
						acc Thr		_				~				1296
	_					gat Asp	_		-	_						1344
_			-			ttg Leu 455			_							1392
						cat His									_	1440
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<211> 509

<212> PRT

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<400> 38

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Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val 35 40 45

Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu 50 55 60

Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val 65 70 75 80

Phe Asp Pro Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly
85 90 95

Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
100 105 110

Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp 115 120 125

Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu 130 135 140

Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu 145 150 155 160

Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr 165 170 175

Leu Thr Leu Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr 180 185 190

Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala 195 200 205

Tyr Glu Leu Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met 210 215 220

Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala 225 230 235 240

Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe

245 250 255

Asn	Val	Asn	Tyr	Thr	Met	His	Tyr	Tyr	Leu	Asn	Asn	Gly	Ala	Thr	Arg
			260					265					270		

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- Glu Asp Arg Ser Lys Val Lys Leu Gly Asp Pro Ala Lys Gly Met Ser 290 295 300
- Pro Pro Gly Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu 305 310 315 320
- Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu 325 330 335
- Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr 340 345 350
- Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu 355 360 365
- Gly Val Ser Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys 370 380
- Gly His Cys Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met 385 390 395 400
- Ile Asn Gly Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser 405 410 415
- Thr Thr Thr Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr 420 425 430
- Pro Thr Pro Thr Thr Thr Asp Ser Thr Ser Glu Thr Pro Lys Tyr Thr
 435 440 445
- Thr Tyr Ile Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu 450 455 460
- Pro His Pro Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala 465 470 475 480
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Thr Arg Trp His Ala Thr Leu Lys Asn Cys Ile Gln Glu

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atcagttgga tgtggaagat aaccttgttt atagcattta atcaaatgtc catcaatata 180
cgtagtgtat tttggtgttt cgcttgtgct atcggtggtg gtaggcgttg gtgtggtagt 240
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gtaagagttc ttttcatcac cattgatcat attgtgaact ttgttcaaca atggatattt 360
cggtccgcaa tgacctttga aatcatcgtt ttccaatgac catatcataa cgccagagac 420
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<213> Dermatophagoides farinae

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	aac Asn										288
	ggt Gly									_	336
	aca Thr 115							-		-	384
	tac Tyr										432
	tta Leu										480
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	gta Val										576

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						ttg Leu 375										1152

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			_	_		agc Ser	_						_			1296
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	Τ.					tgt Cys			_							1470
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Val	Суз	Tyr	Val 20	Gly	Thr	Trp	Ser	Val 25	Tyr	His	Lys	Val	Asp 30	Pro	Tyr	
Thr	Ile	Glu 35	Asp	Ile	Asp	Pro	Phe 40	Lys	Cys	Thr	His	Leu 45	Met	Tyr	Gly	
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Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val Phe Asp Pro

Phe Gln Asp Asp Asn His Asn Ser Trp Glu Lys His Gly Tyr Glu Arg

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Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr Met Ile Ser 85 90 95

Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp Met Ala Ala 100 105 110

Asn Pro Thr Tyr Arg Gln Gln Phe Val Gln Ser Val Leu Asp Phe Leu 115 120 125

Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly 130 135 140

Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr Leu Thr Leu 145 150 155 160

Val Arg Glu Leu Lys Glu Ala Phe Glu Pro Phe Gly Tyr Leu Leu Thr 165 170 175

Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Val Ala Tyr Glu Leu 180 185 190

Lys Glu Leu Asn Gln Leu Phe Asp Trp Met Asn Val Met Thr Tyr Asp 195 200 205

Tyr His Gly Gly Trp Glu Asn Val Phe Gly His Asn Ala Pro Leu Tyr 210 215 220

Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe Asn Val Asn 225 230 235 240

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Phe Ile Thr Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu Leu Cys Gln
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295
300

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Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr Asp Asp Leu

325 330 335

Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu Gly Val Ser 340 345 350

Gly Val Met Ile Trp Ser Leu Glu Asn Asp Asp Phe Lys Gly His Cys 355 360 365

Gly Pro Lys Tyr Pro Leu Leu Asn Lys Val His Asn Met Ile Asn Gly 370 380

Asp Glu Lys Asn Ser Tyr Glu Cys Leu Leu Gly Pro Ser Thr Thr Thr 385 390 395 400

Pro Thr Pro Thr Thr Pro Ser Thr Thr Ser Thr Thr Thr Pro Thr Pro 405 410 415

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420 425 430

Asp Gly His Leu Ile Lys Cys Tyr Lys Gln Gly Tyr Leu Pro His Pro 435 440 445

Thr Asp Val His Lys Tyr Leu Val Cys Glu Tyr Ile Ala Thr Pro Asn 450 455 460

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<211> 1470

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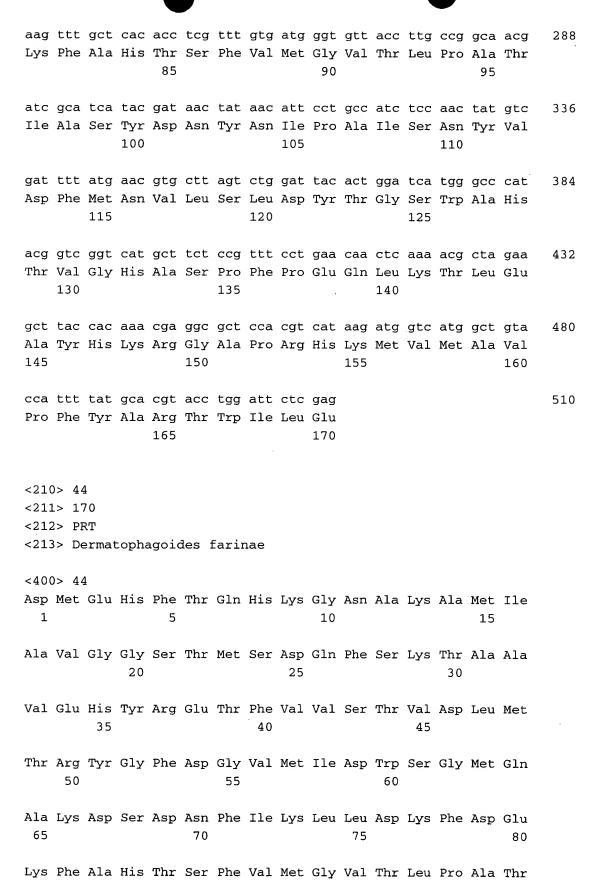


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                                                                   96
Ala Val Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala
             20
                                  25
                                                      30
gta gaa cat tat cgg gaa acg ttt gtt gtt agc aca gtt gat ctt atg
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Val Glu His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met
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                              40
                                                  45
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Thr Arg Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln
     50
                         55
                                              60
gcc aaa gat agt gat aat ttc att aaa ttg ttg gac aaa ttc gac gaa
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Ala Lys Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu
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75

80

70



85 90 95

Ile Ala Ser Tyr Asp Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val 100 105 110

Asp Phe Met Asn Val Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His
115 120 125

Thr Val Gly His Ala Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu 130 135 140

Ala Tyr His Lys Arg Gly Ala Pro Arg His Lys Met Val Met Ala Val 145 150 155 160

Pro Phe Tyr Ala Arg Thr Trp Ile Leu Glu 165 170

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<213> Dermatophagoides farinae

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년 : 1			
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Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala Val Glu His Tyr Arg

110

115

120

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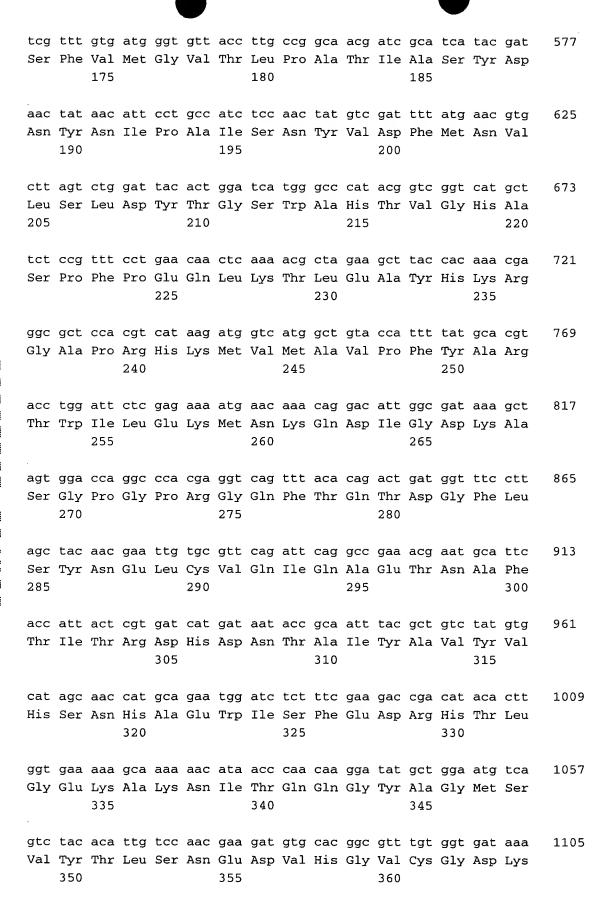
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145

150

155

aat ttc att aaa ttg ttg gac aaa ttc gac gaa aag ttt gct cac acc 529
Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu Lys Phe Ala His Thr
160 165 170



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		_	_		_	atc Ile		_							_	1153
						aca Thr									gaa Glu	1201
						Gly ggc						-	-			1249
						tgt Cys										1297
						acc Thr 435									-	1345
-		_	_	_	_	cgg Arg		_		_						1393
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Cys	Tyr	Tyr 35	Glu	Ser	Trp	Val	His 40	Trp	Arg	Gln	Gly	Glu 45	Gly	Lys	Met	
Asp	Pro 50	Glu	Asp	Ile	Asp	Thr 55	Ser	Leu	Cys	Thr	His 60	Ile	Val	Tyr	Ser	

Tyr Phe Gly Ile Asp Ala Ala Thr His Glu Ile Lys Leu Leu Asp Glu

65 70 75 80

Tyr Leu Met Lys Asp Leu His Asp Met Glu His Phe Thr Gln His Lys
85 90 95

Gly Asn Ala Lys Ala Met Ile Ala Val Gly Gly Ser Thr Met Ser Asp 100 105 110

Gln Phe Ser Lys Thr Ala Ala Val Glu His Tyr Arg Glu Thr Phe Val 115 120 125

Val Ser Thr Val Asp Leu Met Thr Arg Tyr Gly Phe Asp Gly Val Met 130 135 140

Ile Asp Trp Ser Gly Met Gln Ala Lys Asp Ser Asp Asn Phe Ile Lys
145 150 155 160

Leu Leu Asp Lys Phe Asp Glu Lys Phe Ala His Thr Ser Phe Val Met
165 170 175

Gly Val Thr Leu Pro Ala Thr Ile Ala Ser Tyr Asp Asn Tyr Asn Ile 180 185 190

Pro Ala Ile Ser Asn Tyr Val Asp Phe Met Asn Val Leu Ser Leu Asp 195 200 205

Tyr Thr Gly Ser Trp Ala His Thr Val Gly His Ala Ser Pro Phe Pro 210 215 220

Glu Gln Leu Lys Thr Leu Glu Ala Tyr His Lys Arg Gly Ala Pro Arg 225 230 235 240

His Lys Met Val Met Ala Val Pro Phe Tyr Ala Arg Thr Trp Ile Leu 245 250 255

Glu Lys Met Asn Lys Gln Asp Ile Gly Asp Lys Ala Ser Gly Pro Gly
260 265 270

Pro Arg Gly Gln Phe Thr Gln Thr Asp Gly Phe Leu Ser Tyr Asn Glu 275 280 285

Leu Cys Val Gln Ile Gln Ala Glu Thr Asn Ala Phe Thr Ile Thr Arg 290 295 300

Asp His Asp Asn Thr Ala Ile Tyr Ala Val Tyr Val His Ser Asn His 305 310 315 320

Ala Glu Trp Ile Ser Phe Glu Asp Arg His Thr Leu Gly Glu Lys Ala

325 330 335

Lys Asn Ile Thr Gln Gln Gly Tyr Ala Gly Met Ser Val Tyr Thr Leu $340 \hspace{1cm} 345 \hspace{1cm} 350$

Ser Asn Glu Asp Val His Gly Val Cys Gly Asp Lys Asn Pro Leu Leu 355 360 365

His Ala Ile Gln Ser Asn Tyr Tyr His Gly Val Val Thr Glu Pro Thr 370 380

Val Val Thr Leu Pro Pro Val Thr His Thr Thr Glu His Val Thr Asp 385 390 395 400

Ile Pro Gly Val Phe His Cys His Glu Glu Gly Phe Phe Arg Asp Lys 405 410 415

Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys Lys Lys Gly Asp Phe Gly Leu 420 425 430

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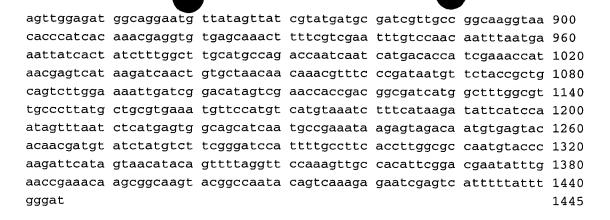
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<212> DNA

<213> Dermatophagoides farinae

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tggcgccaag gtgaaggcaa aatggatccc gaagacatag atacatcgtt gtgtactcac 180
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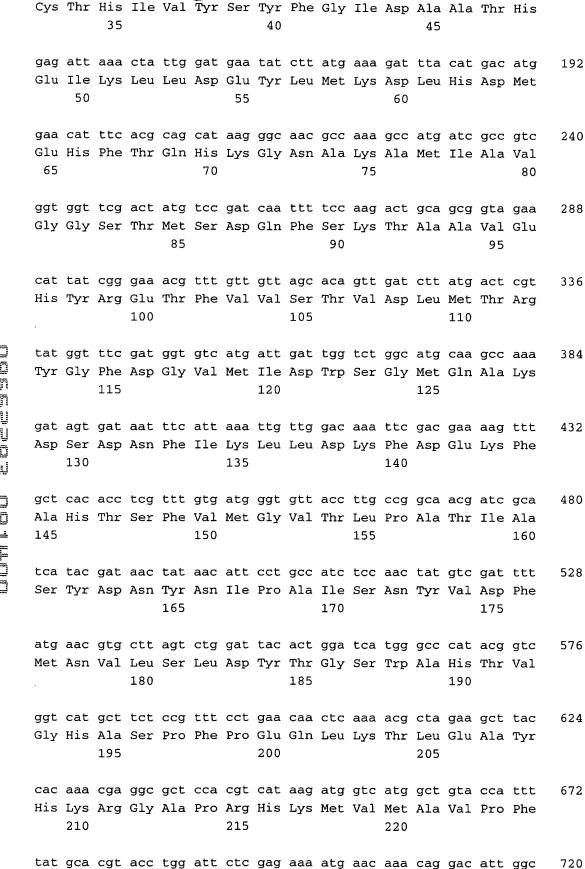
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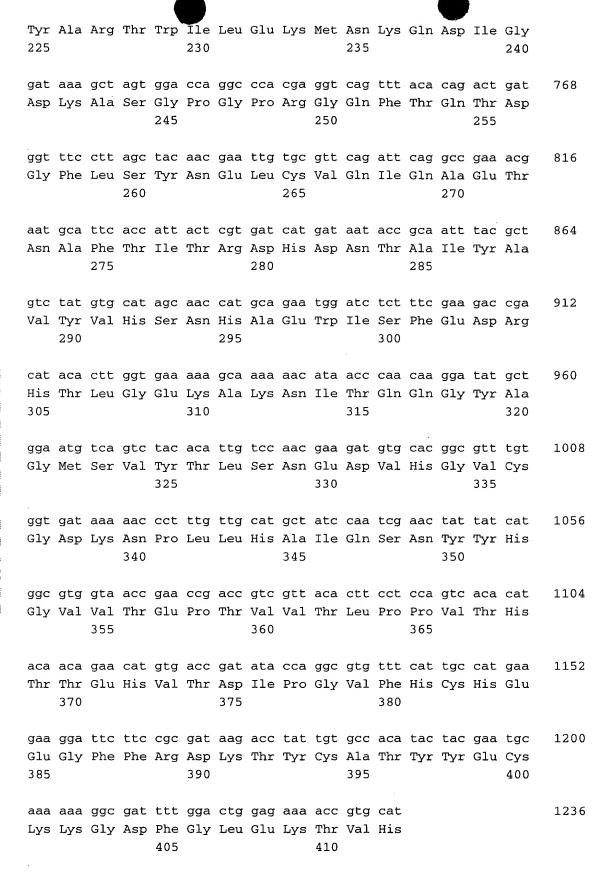
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<213> Dermatophagoides farinae

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                                     10
                                                         15
cgc caa ggt gaa ggc aaa atg gat ccc gaa gac ata gat aca tcg ttg
                                                                   96
Arg Gln Gly Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu
             20
                                 25
tgt act cac att gtc tac tct tat ttc ggc att gat gct gcc act cat
                                                                   144
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<210> 56 <211> 412 <212> PRT <213> Dermatophagoides farinae

Thr Leu Glu Pro Lys Thr Val Cys Tyr Tyr Glu Ser Trp Val His Trp

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Arg Gln Gly Glu Gly Lys Met Asp Pro Glu Asp Ile Asp Thr Ser Leu 20 25 30

Cys Thr His Ile Val Tyr Ser Tyr Phe Gly Ile Asp Ala Ala Thr His 35 40 45

Glu Ile Lys Leu Leu Asp Glu Tyr Leu Met Lys Asp Leu His Asp Met 50 55 60

Glu His Phe Thr Gln His Lys Gly Asn Ala Lys Ala Met Ile Ala Val 65 70 75 80

Gly Gly Ser Thr Met Ser Asp Gln Phe Ser Lys Thr Ala Ala Val Glu 85 90 95

His Tyr Arg Glu Thr Phe Val Val Ser Thr Val Asp Leu Met Thr Arg
100 105 110

Tyr Gly Phe Asp Gly Val Met Ile Asp Trp Ser Gly Met Gln Ala Lys
115 120 125

Asp Ser Asp Asn Phe Ile Lys Leu Leu Asp Lys Phe Asp Glu Lys Phe 130 135 140

Ala His Thr Ser Phe Val Met Gly Val Thr Leu Pro Ala Thr Ile Ala 145 150 155 160

Ser Tyr Asp Asn Tyr Asn Ile Pro Ala Ile Ser Asn Tyr Val Asp Phe 165 170 175

Met Asn Val Leu Ser Leu Asp Tyr Thr Gly Ser Trp Ala His Thr Val 180 185 190

Gly His Ala Ser Pro Phe Pro Glu Gln Leu Lys Thr Leu Glu Ala Tyr 195 200 205

His Lys Arg Gly Ala Pro Arg His Lys Met Val Met Ala Val Pro Phe 210 215 220

Tyr Ala Arg Thr Trp Île Leu Glu Lys Met Asn Lys Gln Asp Ile Gly

240

235

Asp Lys Ala Ser Gly Pro Gly Pro Arg Gly Gln Phe Thr Gln Thr Asp
245
250
255

230

Gly Phe Leu Ser Tyr Asn Glu Leu Cys Val Gln Ile Gln Ala Glu Thr 260 265 270

Asn Ala Phe Thr Ile Thr Arg Asp His Asp Asn Thr Ala Ile Tyr Ala 275 280 285

Val Tyr Val His Ser Asn His Ala Glu Trp Ile Ser Phe Glu Asp Arg 290 295 300

His Thr Leu Gly Glu Lys Ala Lys Asn Ile Thr Gln Gln Gly Tyr Ala 305 310 315 320

Gly Met Ser Val Tyr Thr Leu Ser Asn Glu Asp Val His Gly Val Cys 325 330 335

Gly Asp Lys Asn Pro Leu Leu His Ala Ile Gln Ser Asn Tyr Tyr His 340 345 350

Gly Val Val Thr Glu Pro Thr Val Val Thr Leu Pro Pro Val Thr His 355 360 365

Thr Thr Glu His Val Thr Asp Ile Pro Gly Val Phe His Cys His Glu 370 375 380

Glu Gly Phe Phe Arg Asp Lys Thr Tyr Cys Ala Thr Tyr Tyr Glu Cys 385 390 395 400

Lys Lys Gly Asp Phe Gly Leu Glu Lys Thr Val His 405 410

<210> 57

<211> 1236

<212> DNA

<213> Dermatophagoides farinae

<400> 57

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